



#6

SEQUENCE LISTING

<110> Takara Shuzo Co., Ltd.

<120> DNA POLYMERASES WITH ENHANCED LENGTH OF PRIMER EXTENSION

<130> TKR2050.1

<150> US 08/021,623

<151> 1993-02-19

<150> US 08/483,535

<151> 1995-06-07

<150> US 08/931,818

<151> 1997-09-16

<160> 29

<170> PatentIn version 3.0

<210> 1

<211> 36

<212> DNA

<213> Thermus aquaticus

<220>

<221> CDS

<222> (6) .. (35)

<400> 1

gagcc atg ggc ctc ctc cac gag ttc ggc ctt ctg g
Met Gly Leu Leu His Glu Phe Gly Leu Leu
1 5 10

36

<210> 2

<211> 10

<212> PRT

<213> Thermus aquaticus

<400> 2

Met Gly Leu Leu His Glu Phe Gly Leu Leu
1 5 10

<210> 3

<211> 35

<212> DNA

<213> Thermus aquaticus

<220>

<221> CDS

<222> (2) .. (34)

<400> 3

g gac tgg ctc tcc gcc aag gag tag taa gct tcg c	35
Asp Trp Leu Ser Ala Lys Glu Ala Ser	
1 5	

<210> 4
 <211> 7
 <212> PRT
 <213> *Thermus aquaticus*

<400> 4

Asp Trp Leu Ser Ala Lys Glu
1 5

<210> 5
 <211> 6714
 <212> DNA
 <213> Expression vector

<220>
 <221> CDS
 <222> (1)..(1665)

<400> 5	
atg ggc ctc ctc cac gag ttc ggc ctt ctg gaa agc ccc aag gcc ctg	48
Met Gly Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Lys Ala Leu	
1 5 10 15	

gag gag gcc ccc tgg ccc ccg ccg gaa ggg gcc ttc gtg ggc ttt gtg	96
Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val	
20 25 30	

ctt tcc cgc aag gag ccc atg tgg gcc gat ctt ctg gcc ctg gcc gcc	144
Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala	
35 40 45	

gcc agg ggg ggc cgg gtc cac cgg gcc ccc gag cct tat aaa gcc ctc	192
Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu	
50 55 60	

agg gac ctg aag gag gcg cgg ggg ctt ctc gcc aaa gac ctg agc gtt	240
Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val	
65 70 75 80	

ctg gcc ctg agg gaa ggc ctt ggc ctc ccg ccc ggc gac gac ccc atg	288
Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met	
85 90 95	

ctc ctc gcc tac ctc ctg gac cct tcc aac acc acc ccc gag ggg gtg	336
Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val	
100 105 110	

gcc cgg cgc tac ggc ggg gag tgg acg gag gag gcg ggg gag cgg gcc	384
Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala	
115 120 125	

gcc ctt tcc gag agg ctc ttc gcc aac ctg tgg ggg agg ctt gag ggg Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly 130 135 140	432
gag gag agg ctc ctt tgg ctt tac cgg gag gtg gag agg ccc ctt tcc Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser 145 150 155 160	480
gct gtc ctg gcc cac atg gag gcc acg ggg gtg cgc ctg gac gtg gcc Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala 165 170 175	528
tat ctc agg gcc ttg tcc ctg gag gtg gcc gag gag atc gcc cgc ctc Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu 180 185 190	576
gag gcc gag gtc ttc cgc ctg gcc ggc cac ccc ttc aac ctc aac tcc Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser 195 200 205	624
cgg gac cag ctg gaa agg gtc ctc ttt gac gag cta ggg ctt ccc gcc Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala 210 215 220	672
atc ggc aag acg gag aag acc ggc aag cgc tcc acc agc gcc gcc gtc Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val 225 230 235 240	720
ctg gag gcc ctc cgc gag gcc cac ccc atc gtg gag aag atc ctg cag Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln 245 250 255	768
tac cgg gag ctc acc aag ctg aag agc acc tac att gac ccc ttg ccg Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro 260 265 270	816
gac ctc atc cac ccc agg acg ggc cgc ctc cac acc cgc ttc aac cag Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln 275 280 285	864
acg gcc acg gcc acg ggc agg cta agt agc tcc gat ccc aac ctc cag Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln 290 295 300	912
aac atc ccc gtc cgc acc ccg ctt ggg cag agg atc cgc cgg gcc ttc Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe 305 310 315 320	960
atc gcc gag gag ggg tgg cta ttg gtg gcc ctg gac tat agc cag ata Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile 325 330 335	1008
gag ctc agg gtg ctg gcc cac ctc tcc ggc gac gag aac ctg atc cgg Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg 340 345 350	1056

gtc ttc cag gag ggg cgg gac atc cac acg gag acc gcc agc tgg atg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met 355 360 365	1104
ttc ggc gtc ccc cgg gag gcc gtg gac ccc ctg atg cgc cgg gcg gcc Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala 370 375 380	1152
aag acc atc aac ttc ggg gtc ctc tac ggc atg tcg gcc cac cgc ctc Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu 385 390 395 400	1200
tcc cag gag cta gcc atc cct tac gag gag gcc cag gcc ttc att gag Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu 405 410 415	1248
cgc tac ttt cag agc ttc ccc aag gtg cgg gcc tgg att gag aag acc Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr 420 425 430	1296
ctg gag gag ggc agg agg cgg ggg tac gtg gag acc ctc ttc ggc cgc Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg 435 440 445	1344
cgc cgc tac gtg cca gac cta gag gcc cgg gtg aag agc gtg cgg gag Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu 450 455 460	1392
gcg gcc gag cgc atg gcc ttc aac atg ccc gtc cag ggc acc gcc gcc Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala 465 470 475 480	1440
gac ctc atg aag ctg gct atg gtg aag ctc ttc ccc agg ctg gag gaa Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu Glu 485 490 495	1488
atg ggg gcc agg atg ctc ctt cag gtc cac gac gag ctg gtc ctc gag Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu 500 505 510	1536
gcc cca aaa gag agg gcg gag gcc gtg gcc cgg ctg gcc aag gag gtc Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val 515 520 525	1584
atg gag ggg gtg tat ccc ctg gcc gtg ccc ctg gag gtg gag gtg ggg Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly 530 535 540	1632
ata ggg gag gac tgg ctc tcc gcc aag gag tag taagcttatac gatgataagc Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu 545 550	1685
tggtcaaacat gagaattagc ccgcctaatag agcggggcttt tttttaattc ttgaagacga	1745
aagggcctcg tgatacgcct atttttatag gttaatgtca tgataataat ggtttcttag	1805
cgtcaaagca accatagtagc gcgccctgta gcggcgcatt aagcgcgccg ggtgtggtgg	1865

ttacgcgcag cgtgaccgct acacttgcca gcgccctagc gcccgcctcct ttcgctttct	1925
tcccttcctt tctcgccacg ttcgccggct ttccccgtca agctctaaat cgggggctcc	1985
ctttaggggtt ccgatttagt gctttacggc acctcgaccc caaaaaactt gatttgggtg	2045
atggttcacg tagtgggcca tcgccctgat agacggtttt tcgcccttg acgttgagat	2105
ccacgttctt taatagtgga ctcttggtcc aaacttgaac aacactcaac cctatctcgg	2165
gctattcttt tgatttataa gggattttgc cgatttcggc ctattgggta aaaaatgagc	2225
tgatttaaca aaaatttaac gcgaatttta acaaaatatt aacgtttaca atttcagggtg	2285
gcacttttcg gggaaatgtg cgcggaaccc ctatttggtt atttttctaa atacattcaa	2345
atatgtatcc gctcatgaga caataaccct gataaatgct tcaataatat tgaaaaagga	2405
agagtatgag tattcaacat ttccgtgtcg cccttattcc cttttttgcg gcattttgcc	2465
ttcctgtttt tgctcaccca gaaacgctgg tgaaagtaaa agatgctgaa gatcagttgg	2525
gtgcacgagt gggttacatc gaactggatc tcaacagcgg taagatcctt gagagttttc	2585
gccccgaaga acgttttcca atgatgagca cttttaaaagt tctgctatgt ggcgcggtat	2645
tatcccggtg tgacgcggg caagagcaac tcggtcgccg catacactat tctcagaatg	2705
acttggttga gtactcacca gtcacagaaa agcatcttac ggatggcatg acagtaagag	2765
aattatgcag tgctgccata accatgagtg ataacactgc ggccaactta cttctgacaa	2825
cgatcggagg accgaaggag ctaaccgctt ttttgacaaa catgggggat catgtaactc	2885
gccttgatcg ttgggaaccg gagctgaatg aagccatacc aaacgacgag cgtgacacca	2945
cgatgcctgc agcaatggca acaacgttgc gcaaactatt aactggcgaa ctacttactc	3005
tagcttcccg gcaacaatta atagactgga tggaggcgga taaagttgca ggaccacttc	3065
tgcgctcggc ccttcgggtt ggctggttta ttgctgataa atctggagcc ggtgagcgtg	3125
ggtctcgcgg tatcattgca gcactggggc cagatggtaa gccctcccg atcgtagtta	3185
tctacacgac ggggagtcag gcaactatgg atgaacgaaa tagacagatc gctgagatag	3245
gtgcctcact gattaagcat tggttaactgt cagaccaagt ttactcatat atactttaga	3305
ttgatttaaa acttcatttt taatttaaaa ggatctaggt gaagatcctt tttgataatc	3365
tcatgaccaa aatcccttaa cgtgagtttt cgttcactg agcgtcagac cccgtagaaa	3425
agatcaaagg atcttcttga gatccttttt ttctgcgcgt aatctgctgc ttgcaaacaa	3485
aaaaaccacc gctaccagcg gtggtttgtt tgccggatca agagctacca actctttttc	3545



egaaggtaac tggcttcagc agagcgcaga taccaaatac tgtccttcta gtgtagccgt	3605
agttaggcca ccacttcaag aactctgtag caccgcctac atacctcgct ctgctaatacc	3665
tgttaccagt ggctgctgcc agtggcgata agtcgtgtct taccgggttg gactcaagac	3725
gatagttacc ggataaggcg cagcggctcg gctgaacggg gggttcgtgc acacagccca	3785
gcttggagcg aacgacctac accgaactga gataacctaca gcgtgagcta tgagaaagcg	3845
ccacgcttcc cgaagggaga aaggcggaca ggtatccggt aagcggcagg gtcggaacag	3905
gagagcgcac gaggagctt ccagggggaa acgcctggta tctttatagt cctgtcgggt	3965
ttcgccacct ctgacttgag cgtcgatttt tgtgatgctc gtcagggggg cggagcctat	4025
ggaaaaacgc cagcaacgcg gcctttttac ggttcctggc cttttgctgg ccttttgctc	4085
acatgttctt tcttgcgtta tcccctgatt ctgtggataa ccgtattacc gcctttgagt	4145
gagctgatac cgctcgccgc agccgaacga ccgagcgcag cgagtcagtg agcgaggaag	4205
cggaagagcg cctgatgcgg tattttctcc ttacgcactt gtgcgggtatt tcacaccgca	4265
tatggtgcac tctcagtaca atctgctctg atgccgcata gttaagccag tatacactcc	4325
gctatcgcta cgtgactggg tcatggctgc gccccgacac ccgccaacac ccgctgacgc	4385
gccctgacgg gcttgtctgc tcccggcatc cgcttacaga caagctgtga ccgtctccgg	4445
gagctgcatg tgtcagaggt ttccaccgtc atcaccgaaa cgcgcgaggc agaacgccat	4505
caaaaataat tcgcgtctgg ccttcctgta gccagctttc atcaacatta aatgtgagcg	4565
agtaacaacc cgtcggattc tccgtgggaa caaacggcgg attgaccgta atgggatagg	4625
ttacgttggg gtagatgggc gcatcgtaac cgtgcatctg ccagtttgag gggacgacga	4685
cagtatcggc ctcaggaaga tcgcactcca gccagctttc cggcaccgct tctggtgccg	4745
gaaaccaggc aaagcgccat tcgccattca ggctgcgcaa ctgttgggaa gggcgatcgg	4805
tgcgggcctc ttcgctatta cgccagctgg cgaaaggggg atgtgctgca aggcgattaa	4865
gttgggtaac gccagggttt tcccagtcac gacgttgtaa aacgacggcc agtgaatccg	4925
taatcatggg catagctgtt tctgtgtgta aattgttatc cgctcacaat tccacacaac	4985
atacgagccg gaagcataaa gtgtaaagcc tgggggtgcct aatgagtgag ctaactcaca	5045
ttaattgctg tcgcctcact gcccgccttc cagtcgggaa acctgtcgtg ccagctgcat	5105
taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgcca gggtggtttt	5165
tcttttcacc agtgagacgg gcaacagctg attgcccttc accgcctggc cctgagagag	5225
ttgcagcaag cgggtccacgc tggtttgccc cagcaggcga aaatcctggt tgatggtggt	5285



tgacggcggg atataacatg agctgtcttc ggtatcgtcg tatcccacta ccgagatatc	5345
cgcaccaacg cgcagcccgg actcggtaat ggcgcgcatt gcgccagcg ccatctgac	5405
gttggaacc agcatcgcag tgggaacgat gccctcattc agcatttgca tggtttggtg	5465
aaaaccggac atggcactcc agtcgccttc ccgttcgct atcggctgaa tttgattgcg	5525
agtgagatat ttatgccagc cagccagacg cagacgcgcc gagacagaac ttaatgggcc	5585
cgctaacagc gcgatttgct ggtgaccaa tgcgaccaga tgctccacgc ccagtcgcgt	5645
accgtcttca tgggagaaaa taatactggt gatgggtgtc tggtcagaga catcaagaaa	5705
taacgccgga acattagtgc aggacgcttc cacagcaatg gcacctggt catccagcg	5765
atagttaatg atcagcccac tgacgcgttg cgcgagaaga ttgtgcaccg ccgctttaca	5825
ggcttcgacg ccgcttcggt ctaccatcga caccaccacg ctggcaccca gttgatcggc	5885
gcgagattta atcgccgcga caatttgca cggcgcgtgc agggccagac tggaggtggc	5945
aacgccaatc agcaacgact gtttgccgc cagttgttgt gccacgcggt tgggaatgta	6005
attcagctcc gccatcgccg cttccacttt ttcccgcgtt ttcgcagaaa cgtggctggc	6065
ctggttcacc acgcgggaaa cggcttgata agagacaccg gcatactctg cgacatcgta	6125
taacgttact ggtttcacat tcaccacct gaattgactc tcttcgggc gctatcatgc	6185
cataccgcga aagggtttgc gccattogat ggtgtcccag tgaatccgta atcatggtca	6245
tagctgtttc ctgtgtgaaa ttgttatccg ctcacaattc cacacattat acgagccgga	6305
agcataaagt gtaaagcctg ggggtgcctaa tgagtgaagt aactcacatt aattgcgttg	6365
cgctcactgc ccgctttcca gtcgggaaac ctgtcgtgcc agctgcatta atgaatcgga	6425
gcttactccc catccccctg ttgacaatta atcatcggt cgtataatgt gtggaattgt	6485
gagcggataa caatttcaca caggaaacag gatcgatcca gcttactccc catccccctg	6545
ttgacaatta atcatcggt cgtataatgt gtggaattgt gagcggataa caatttcaca	6605
caggaaacag gatctgggcc cttcgaaatt aatacgactc actatagga gaccacaacg	6665
gtttccctct agaaataatt ttgtttaact ttaagaagga gatatatcc	6714

<210> 6
 <211> 554
 <212> PRT
 <213> Expression vector

 <400> 6

Met Gly Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Lys Ala Leu
1 5 10 15

Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val
20 25 30

Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala
35 40 45

Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu
50 55 60

Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val
65 70 75 80

Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met
85 90 95

Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val
100 105 110

Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala
115 120 125

Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly
130 135 140

Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser
145 150 155 160

Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala
165 170 175

Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu
180 185 190

Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser
195 200 205

Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala
210 215 220

Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val

225		230		235		240
Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln						
	245			250		255
Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro						
	260			265		270
Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln						
	275			280		285
Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln						
	290			295		300
Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe						
305		310		315		320
Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile						
	325			330		335
Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg						
	340			345		350
Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met						
	355			360		365
Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala						
370		375		380		
Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu						
385		390		395		400
Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu						
	405			410		415
Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr						
	420			425		430
Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg						
	435			440		445
Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu						
	450			455		460

Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala
 465 470 475 480

Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu Glu
 485 490 495

Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu
 500 505 510

Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val
 515 520 525

Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly
 530 535 540

Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
 545 550

<210> 7
 <211> 27
 <212> DNA
 <213> Bacteriophage lambda

<400> 7
 gcttatctgc ttctcataga gtcttgc 27

<210> 8
 <211> 27
 <212> DNA
 <213> Bacteriophage lambda

<400> 8
 ataacgatca tatacatggt tctctcc 27

<210> 9
 <211> 27
 <212> DNA
 <213> Bacteriophage lambda

<400> 9
 ttttgctggg tcaggttggt ctttagg 27

<210> 10
 <211> 28
 <212> DNA
 <213> Escherichia coli

<400> 10	
ggaagcttat ttttgacacc agaccaac	28
<210> 11	
<211> 37	
<212> DNA	
<213> Zea mays	
<400> 11	
gtgatggatc cttcagcttc ccgagttcag caggcgg	37
<210> 12	
<211> 37	
<212> DNA	
<213> Zea mays	
<400> 12	
ggtctcgagc gaagcttccc tatagctttg cgaagag	37
<210> 13	
<211> 37	
<212> DNA	
<213> Thermus aquaticus	
<400> 13	
gagccatggc caacctgtgg gggaggcttg aggggga	37
<210> 14	
<211> 36	
<212> DNA	
<213> Thermus aquaticus	
<400> 14	
agtttggcag cctcctccac gagttcggcc ttctgg	36
<210> 15	
<211> 32	
<212> DNA	
<213> Thermus aquaticus	
<400> 15	
ggactggctc tccgccaagg agtgatacca cc	32
<210> 16	
<211> 36	
<212> DNA	
<213> Thermus flavis	
<400> 16	
agtttgaag cctcctccac gagttcggcc tcttgg	36

<210> 17
 <211> 35
 <212> DNA
 <213> *Thermus flavis*

 <400> 17
 ggactggctc tccgccaagg agtagggggg tcctg 35

<210> 18
 <211> 39
 <212> DNA
 <213> *Bacillus thuringiensis*

 <400> 18
 gcgaagcttc tcgagttacg ctcaatatgg agttgcttc 39

<210> 19
 <211> 43
 <212> DNA
 <213> *Bacillus thuringiensis*

 <400> 19
 ccgagatctc catggatcca aagaatcaag ataagcatca aag 43

<210> 20
 <211> 36
 <212> DNA
 <213> *Bacteriophage lambda*

 <400> 20
 gggcgggcgac ctgcggggtt ttcgctatct atgaaa 36

<210> 21
 <211> 33
 <212> DNA
 <213> *Escherichia coli*

 <400> 21
 cgacggccag tgaatccgta atcatggtca tag 33

<210> 22
 <211> 33
 <212> DNA
 <213> *Escherichia coli*

 <400> 22
 accagccatc gccatctgct gcacgcggaa gaa 33

<210> 23

<211> 36
 <212> DNA
 <213> Escherichia coli

 <400> 23
 ctatgaccat gattacggat tcactggccg tcgttt 36

 <210> 24
 <211> 33
 <212> DNA
 <213> Bacteriophage lambda

 <400> 24
 gcaagactct atgagaagca gataagcgat aag 33

 <210> 25
 <211> 33
 <212> DNA
 <213> Bacteriophage lambda

 <400> 25
 atcattatatt gatttcaatt ttgtcccact ccc 33

 <210> 26
 <211> 33
 <212> DNA
 <213> Bacteriophage lambda

 <400> 26
 ggagagaacc atgtatatga tcgttatctg ggt 33

 <210> 27
 <211> 33
 <212> DNA
 <213> Bacteriophage lambda

 <400> 27
 gcgcacaaaa ccatagattg ctcttctgta agg 33

 <210> 28
 <211> 33
 <212> DNA
 <213> Escherichia coli

 <400> 28
 cccggttatt attatTTTTg acaccagacc aac 33

 <210> 29
 <211> 36
 <212> DNA
 <213> Bacteriophage lambda

<400> 29

aggtcgccgc cccgtaacct gtcggatcac cggaaa

36

SEQUENCE LISTING

<110> Takara Shuzo Co., Ltd.

<120> DNA POLYMERASES WITH ENHANCED LENGTH OF PRIMER EXTENSION

<130> TKR2050.1

<150> US 08/021,623

<151> 1993-02-19

<150> US 08/483,535

<151> 1995-06-07

<150> US 08/931,818

<151> 1997-09-16

<160> 29

<170> PatentIn version 3.0

<210> 1

<211> 36

<212> DNA

<213> Thermus aquaticus

<220>

<221> CDS

<222> (6)..(35)

<400> 1

gagcc atg ggc ctc ctc cac gag ttc ggc ctt ctg g
Met Gly Leu Leu His Glu Phe Gly Leu Leu
1 5 10

36

<210> 2

<211> 10

<212> PRT

<213> Thermus aquaticus

<400> 2

Met Gly Leu Leu His Glu Phe Gly Leu Leu
1 5 10

<210> 3

<211> 35

<212> DNA

<213> Thermus aquaticus

<220>

<221> CDS

<222> (2)..(34)

<400> 3

g gac tgg ctc tcc gcc aag gag tag taa gct tcg c	35
Asp Trp Leu Ser Ala Lys Glu Ala Ser	
1 5	

<210> 4
 <211> 7
 <212> PRT
 <213> *Thermus aquaticus*

<400> 4

Asp Trp Leu Ser Ala Lys Glu
1 5

<210> 5
 <211> 6714
 <212> DNA
 <213> Expression vector

<220>
 <221> CDS
 <222> (1)..(1665)

<400> 5 atg ggc ctc ctc cac gag ttc ggc ctt ctg gaa agc ccc aag gcc ctg Met Gly Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Lys Ala Leu 1 5 10 15	48
gag gag gcc ccc tgg ccc ccg ccg gaa ggg gcc ttc gtg ggc ttt gtg Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val 20 25 30	96
ctt tcc cgc aag gag ccc atg tgg gcc gat ctt ctg gcc ctg gcc gcc Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala 35 40 45	144
gcc agg ggg ggc cgg gtc cac cgg gcc ccc gag cct tat aaa gcc ctc Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu 50 55 60	192
agg gac ctg aag gag gcg cgg ggg ctt ctc gcc aaa gac ctg agc gtt Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val 65 70 75 80	240
ctg gcc ctg agg gaa ggc ctt ggc ctc ccg ccc ggc gac gac ccc atg Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met 85 90 95	288
ctc ctc gcc tac ctc ctg gac cct tcc aac acc acc ccc gag ggg gtg Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val 100 105 110	336
gcc cgg cgc tac ggc ggg gag tgg acg gag gag gcg ggg gag cgg gcc Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala 115 120 125	384

gcc ctt tcc gag agg ctc ttc gcc aac ctg tgg ggg agg ctt gag ggg Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly 130 135 140	432
gag gag agg ctc ctt tgg ctt tac cgg gag gtg gag agg ccc ctt tcc Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser 145 150 155 160	480
gct gtc ctg gcc cac atg gag gcc acg ggg gtg cgc ctg gac gtg gcc Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala 165 170 175	528
tat ctc agg gcc ttg tcc ctg gag gtg gcc gag gag atc gcc cgc ctc Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu 180 185 190	576
gag gcc gag gtc ttc cgc ctg gcc ggc cac ccc ttc aac ctc aac tcc Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser 195 200 205	624
cgg gac cag ctg gaa agg gtc ctc ttt gac gag cta ggg ctt ccc gcc Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala 210 215 220	672
atc ggc aag acg gag aag acc ggc aag cgc tcc acc agc gcc gcc gtc Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val 225 230 235 240	720
ctg gag gcc ctc cgc gag gcc cac ccc atc gtg gag aag atc ctg cag Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln 245 250 255	768
tac cgg gag ctc acc aag ctg aag agc acc tac att gac ccc ttg ccg Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro 260 265 270	816
gac ctc atc cac ccc agg acg ggc cgc ctc cac acc cgc ttc aac cag Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln 275 280 285	864
acg gcc acg gcc acg ggc agg cta agt agc tcc gat ccc aac ctc cag Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln 290 295 300	912
aac atc ccc gtc cgc acc ccg ctt ggg cag agg atc cgc cgg gcc ttc Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe 305 310 315 320	960
atc gcc gag gag ggg tgg cta ttg gtg gcc ctg gac tat agc cag ata Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile 325 330 335	1008
gag ctc agg gtg ctg gcc cac ctc tcc ggc gac gag aac ctg atc cgg Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg 340 345 350	1056

gtc ttc cag gag ggg cgg gac atc cac acg gag acc gcc agc tgg atg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met 355 360 365	1104
ttc ggc gtc ccc cgg gag gcc gtg gac ccc ctg atg cgc cgg gcg gcc Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala 370 375 380	1152
aag acc atc aac ttc ggg gtc ctc tac ggc atg tcg gcc cac cgc ctc Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu 385 390 395 400	1200
tcc cag gag cta gcc atc cct tac gag gag gcc cag gcc ttc att gag Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu 405 410 415	1248
cgc tac ttt cag agc ttc ccc aag gtg cgg gcc tgg att gag aag acc Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr 420 425 430	1296
ctg gag gag ggc agg agg cgg ggg tac gtg gag acc ctc ttc ggc cgc Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg 435 440 445	1344
cgc cgc tac gtg cca gac cta gag gcc cgg gtg aag agc gtg cgg gag Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu 450 455 460	1392
gcg gcc gag cgc atg gcc ttc aac atg ccc gtc cag ggc acc gcc gcc Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala 465 470 475 480	1440
gac ctc atg aag ctg gct atg gtg aag ctc ttc ccc agg ctg gag gaa Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu Glu 485 490 495	1488
atg ggg gcc agg atg ctc ctt cag gtc cac gac gag ctg gtc ctc gag Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu 500 505 510	1536
gcc cca aaa gag agg gcg gag gcc gtg gcc cgg ctg gcc aag gag gtc Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val 515 520 525	1584
atg gag ggg gtg tat ccc ctg gcc gtg ccc ctg gag gtg gag gtg ggg Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly 530 535 540	1632
ata ggg gag gac tgg ctc tcc gcc aag gag tag taagcttatac gatgataagc Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu 545 550	1685
tgtcaaacat gagaattagc ccgcctaatag agcgggcttt tttttaattc ttgaagacga	1745
aagggcctcg tgatacgccct atttttatag gttaatgtca tgataataat ggtttcttag	1805
cgtcaaagca accatagtac gcgccctgta gcggcgccatt aagcgcgccg ggtgtggtgg	1865

ttacgcgcag cgtgaccgct acacttgcca ggcgcctagc gcccgctcct ttcgctttct	1925
tcccttcctt tctcgccacg ttcgccggct ttccccgtca agctctaaat cgggggctcc	1985
ctttaggggtt ccgatttagt gctttacggc acctcgaccc caaaaaactt gatttgggtg	2045
atgggtcacg tagtgggcca tcgccctgat agacggtttt tcgcccttg acgttggagt	2105
ccacgttctt taatagtgga ctcttggtcc aaacttgaac aacactcaac cctatctcg	2165
gctattcttt tgatttataa gggattttgc cgatttcggc ctattgggta aaaaatgagc	2225
tgatttaaca aaaatttaac gcgaatttta acaaaatatt aacgtttaca atttcaggtg	2285
gcacttttcg gggaaatgtg cgcggaaccc ctatttggtt atttttctaa atacattcaa	2345
atatgtatcc gctcatgaga caataaccct gataaatgct tcaataatat tgaaaaagga	2405
agagtatgag tattcaacat ttccgtgtcg cccttattcc cttttttgcg gcattttgcc	2465
ttcctgtttt tgctcaccca gaaacgctgg tgaaagtaaa agatgctgaa gatcagttgg	2525
gtgcacgagt gggttacatc gaactggatc tcaacagcgg taagatcctt gagagttttc	2585
gccccgaaga acgttttcca atgatgagca cttttaaggt tctgctatgt ggcgcggtat	2645
tatcccggtg tgacgcggg caagagcaac tcggtcgccg catacactat tctcagaatg	2705
acttggttga gtactacca gtcacagaaa agcatcttac ggatggcatg acagtaagag	2765
aattatgcag tgctgccata accatgagtg ataacactgc ggccaactta cttctgacaa	2825
cgatcggagg accgaaggag ctaaccgctt ttttgacaaa catgggggat catgtaactc	2885
gccttgatcg ttgggaaccg gagctgaatg aagccatacc aaacgacgag cgtgacacca	2945
cgatgcctgc agcaatggca acaacgttgc gcaaactatt aactggcgaa ctacttactc	3005
tagcttcccg gcaacaatta atagactgga tggaggcgga taaagttgca ggaccacttc	3065
tgcgctcggc ccttcgggtt ggctggttta ttgctgataa atctggagcc ggtgagcgtg	3125
ggtctcgcgg tatcattgca gcaactgggc cagatggtaa gccctcccg atcgtagtta	3185
tctacacgac ggggagtcag gcaactatgg atgaacgaaa tagacagatc gctgagatag	3245
gtgcctcact gattaagcat tggtaactgt cagaccaagt ttactcatat atactttaga	3305
ttgatttaaa acttcatttt taatttaaaa ggatctaggt gaagatcctt tttgataatc	3365
tcatgaccaa aatcccttaa cgtgagtttt cgttccactg agcgtcagac cccgtagaaa	3425
agatcaaagg atcttcttga gatccttttt ttctgcgcgt aatctgctgc ttgcaaacaa	3485
aaaaaccacc gctaccagcg gtggtttgtt tgccggatca agagctacca actctttttc	3545

cgaaggtaac tggcttcagc agagcgcaga taccaaatac tgtccttcta gtgtagccgt	3605
agttaggcca ccacttcaag aactctgtag caccgcctac atacctcgct ctgctaatacc	3665
tgttaccagt ggctgctgcc agtggcgata agtcgtgtct taccgggttg gactcaagac	3725
gatagttacc ggataaggcg cagcggtcgg gctgaacggg gggttcgtgc acacagccca	3785
gcttggagcg aacgacctac accgaactga gataacctaca gcgtgagcta tgagaaagcg	3845
ccacgcttcc cgaagggaga aaggcggaca ggtatccggt aagcggcagg gtcggaacag	3905
gagagcgcac gagggagctt ccagggggaa acgcctggta tctttatagt cctgtcgggt	3965
ttcgccacct ctgacttgag cgtcgatttt tgtgatgctc gtcagggggg cggagcctat	4025
ggaaaaacgc cagcaacgcg gcctttttac ggttcctggc cttttgctgg ccttttgctc	4085
acatgttctt tctcgctta tcccctgatt ctgtggataa ccgtattacc gcctttgagt	4145
gagctgatac cgctcgccgc agccgaacga ccgagcgcag cgagtcagtg agcgaggaag	4205
cggaagagcg cctgatgcgg tattttctcc ttacgcattc gtgcggtatt tcacaccgca	4265
tatggtgcac tctcagtaca atctgctctg atgccgcata gttaagccag tatacactcc	4325
gctatcgcta cgtgactggg tcatggctgc gccccgacac ccgccaacac ccgctgacgc	4385
gccctgacgg gcttgtctgc tcccggcatc cgcttacaga caagctgtga ccgtctccgg	4445
gagctgcatg tgtcagaggt ttccaccgtc atcaccgaaa cgcgcgaggc agaacgccat	4505
caaaaataat tcgctctgg ccttcctgta gccagctttc atcaacatta aatgtgagcg	4565
agtaacaacc cgtcggattc tccgtgggaa caaacggcgg attgaccgta atgggatagg	4625
ttacgttggg gtagatgggc gcatcgtaac cgtgcatctg ccagtttgag gggacgacga	4685
cagtatcggc ctcaggaaga tcgcactcca gccagctttc cggcaccgct tctggtgccg	4745
gaaaccaggc aaagcgccat tcgccattca ggctgcgcaa ctgttgggaa gggcgatcgg	4805
tgcgggcctc ttcgctatta cgccagctgg cgaaaggggg atgtgctgca aggcgattaa	4865
gttgggtaac gccagggttt tcccagtcac gacgttgtaa aacgacggcc agtgaatccg	4925
taatcatggg catagctggt tctgtgtgta aattgttata cgctcacaat tccacacaac	4985
atacgagccg gaagcataaa gtgtaaagcc tgggggtgcct aatgagtgag ctaactcaca	5045
ttaattgcgt tgcgctcact gcccgctttc cagtcgggaa acctgtcgtg ccagctgcat	5105
taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgcca ggggtggtttt	5165
tcttttcacc agtgagacgg gcaacagctg attgcccttc accgcctggc cctgagagag	5225
ttgcagcaag cgggtccacgc tggtttgccc cagcaggcga aaatcctgtt tgatggtggt	5285

tgacggcggg atataacatg agctgtcttc ggtatcgctg tatccacta ccgagatatc	5345
cgcaccaacg cgcagcccgg actcggtaat ggcgcgcatt gcgcccagcg ccatctgac	5405
gttggcaacc agcatcgcag tgggaacgat gccctcatte agcatttgca tggtttggtg	5465
aaaaccggac atggcactcc agtcgccttc ccgttcgct atcggctgaa tttgattgcg	5525
agtgagatat ttatgccagc cagccagacg cagacgcgcc gagacagaac ttaatgggcc	5585
cgctaacagc gcgatttgct ggtgacccaa tgcgaccaga tgctccacgc ccagtcgcgt	5645
accgtcttca tgggagaaaa taatactggt gatgggtgtc tggtcagaga catcaagaaa	5705
taacgccgga acattagtgc aggcagcttc cacagcaatg gcatcctggt catccagcgg	5765
atagttaatg atcagcccac tgacgcgttg cgcgagaaga ttgtgcaccg ccgctttaca	5825
ggcttcgacg ccgcttcggt ctaccatoga caccaccacg ctggcaccca gttgatcggc	5885
gcgagattta atcgccgcga caatttgoga cggcgcgtgc agggccagac tggaggtggc	5945
aacgccaatc agcaacgact gtttgccgc cagttgttgt gccacgcggt tgggaatgta	6005
attcagctcc gccatgcgcg cttccacttt ttcccgcgtt ttcgcagaaa cgtggctggc	6065
ctggttcacc acgcgggaaa cggctgata agagacaccg gcatactctg cgacatcgta	6125
taacgttact ggtttcacat tcaccacct gaattgactc tcttcgggc gctatcatgc	6185
cataccgcga aaggttttgc gccattcgat ggtgtcccag tgaatccgta atcatggtca	6245
tagctgtttc ctgtgtgaaa ttgttatccg ctcacaattc cacacattat acgagccgga	6305
agcataaagt gttaaagcctg ggggtgcctaa tgagtgagct aactcacatt aattgcgttg	6365
cgctcactgc ccgctttcca gtcgggaaac ctgtcgtgcc agctgcatta atgaatcgga	6425
gcttactccc catccccctg ttgacaatta atcatcggct cgtataatgt gtggaattgt	6485
gagcggataa caatttcaca caggaaacag gatcgatcca gcttactccc catccccctg	6545
ttgacaatta atcatcggct cgtataatgt gtggaattgt gagcggataa caatttcaca	6605
caggaaacag gatctgggcc cttcgaaatt aatacgactc actataggga gaccacaacg	6665
gtttccctct agaaataatt ttgtttaact ttaagaagga gatatatcc	6714

<210> 6
 <211> 554
 <212> PRT
 <213> Expression vector
 <400> 6

Met Gly Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Lys Ala Leu
1 5 10 15

Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val
20 25 30

Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala
35 40 45

Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu
50 55 60

Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val
65 70 75 80

Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met
85 90 95

Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val
100 105 110

Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala
115 120 125

Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly
130 135 140

Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser
145 150 155 160

Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala
165 170 175

Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu
180 185 190

Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser
195 200 205

Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala
210 215 220

Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val

225		230		235		240
Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln						
	245			250		255
Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro						
	260			265		270
Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln						
	275			280		285
Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln						
	290			295		300
Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe						
305		310		315		320
Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile						
	325			330		335
Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg						
	340			345		350
Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met						
	355			360		365
Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala						
370		375		380		
Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu						
385		390		395		400
Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu						
	405			410		415
Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr						
	420			425		430
Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg						
	435			440		445
Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu						
450		455		460		

Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala
 465 470 475 480

Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu Glu
 485 490 495

Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu
 500 505 510

Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val
 515 520 525

Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly
 530 535 540

Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
 545 550

<210> 7
 <211> 27
 <212> DNA
 <213> Bacteriophage lambda

<400> 7
 gcttatctgc ttctcataga gtcttgc 27

<210> 8
 <211> 27
 <212> DNA
 <213> Bacteriophage lambda

<400> 8
 ataacgatca tatacatggt tctctcc 27

<210> 9
 <211> 27
 <212> DNA
 <213> Bacteriophage lambda

<400> 9
 ttttgctggg tcagggtggt ctttagg 27

<210> 10
 <211> 28
 <212> DNA
 <213> Escherichia coli

<400> 10
 ggaagcttat ttttgacacc agaccaac 28

<210> 11
 <211> 37
 <212> DNA
 <213> Zea mays

<400> 11
 gtgatggatc cttcagcttc ccgagttcag cagggcgg 37

<210> 12
 <211> 37
 <212> DNA
 <213> Zea mays

<400> 12
 ggtctcgagc gaagcttccc tatagctttg cgaagag 37

<210> 13
 <211> 37
 <212> DNA
 <213> Thermus aquaticus

<400> 13
 gagccatggc caacctgtgg gggaggcttg aggggga 37

<210> 14
 <211> 36
 <212> DNA
 <213> Thermus aquaticus

<400> 14
 agtttggcag cctcctccac gagttcggcc ttctgg 36

<210> 15
 <211> 32
 <212> DNA
 <213> Thermus aquaticus

<400> 15
 ggactggctc tccgccaagg agtgatacca cc 32

<210> 16
 <211> 36
 <212> DNA
 <213> Thermus flavis

<400> 16
 agtttgggaag cctcctccac gagttcggcc tcctgg 36

<210> 17
 <211> 35
 <212> DNA
 <213> *Thermus flavis*

 <400> 17
 ggactggctc tccgccaagg agtagggggg tcctg 35

 <210> 18
 <211> 39
 <212> DNA
 <213> *Bacillus thuringiensis*

 <400> 18
 gcgaagcttc tcgagttacg ctcaatatgg agttgcttc 39

 <210> 19
 <211> 43
 <212> DNA
 <213> *Bacillus thuringiensis*

 <400> 19
 ccgagatctc catggatcca aagaatcaag ataagcatca aag 43

 <210> 20
 <211> 36
 <212> DNA
 <213> Bacteriophage lambda

 <400> 20
 gggcgggcgac ctgcggggtt ttcgctatatt atgaaa 36

 <210> 21
 <211> 33
 <212> DNA
 <213> *Escherichia coli*

 <400> 21
 cgacggccag tgaatccgta atcatgggtca tag 33

 <210> 22
 <211> 33
 <212> DNA
 <213> *Escherichia coli*

 <400> 22
 accagccatc gccatctgct gcacgcggaa gaa 33

 <210> 23

<211> 36
 <212> DNA
 <213> Escherichia coli

 <400> 23
 ctatgacat gattacggat tcactggccg tcgttt 36

 <210> 24
 <211> 33
 <212> DNA
 <213> Bacteriophage lambda

 <400> 24
 gcaagactct atgagaagca gataagcgat aag 33

 <210> 25
 <211> 33
 <212> DNA
 <213> Bacteriophage lambda

 <400> 25
 atcattatct gatttcaatt ttgtcccact ccc 33

 <210> 26
 <211> 33
 <212> DNA
 <213> Bacteriophage lambda

 <400> 26
 ggagagaacc atgtatatga tcgttatctg ggt 33

 <210> 27
 <211> 33
 <212> DNA
 <213> Bacteriophage lambda

 <400> 27
 gcgcacaaaa ccatagattg ctcttctgta agg 33

 <210> 28
 <211> 33
 <212> DNA
 <213> Escherichia coli

 <400> 28
 cccggttatt attatttttg acaccagacc aac 33

 <210> 29
 <211> 36
 <212> DNA
 <213> Bacteriophage lambda

<400> 29

aggtcgccgc cccgtaacct gtcggatcac cggaaa

36